

# Kunchithapadam Swaminathan

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

2,449  
citations

236925

25  
h-index

206112

48  
g-index

57  
all docs

57  
docs citations

57  
times ranked

4476  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and functional analyses of the PPlase domain of <i>Arabidopsis thaliana</i> CYP71 reveal its catalytic activity toward histone H3. <i>FEBS Letters</i> , 2021, 595, 145-154.	2.8	4
2	Molecular modeling and interaction between <i>Arabidopsis</i> sulfite oxidase and the GW motif of Turnip crinkle virus coat protein. <i>Virology</i> , 2020, 551, 64-74.	2.4	2
3	A feedforward relationship between active Rac1 and phosphorylated Bcl-2 is critical for sustaining Bcl-2 phosphorylation and promoting cancer progression. <i>Cancer Letters</i> , 2019, 457, 151-167.	7.2	20
4	Engineering of serine protease for improved thermostability and catalytic activity using rational design. <i>International Journal of Biological Macromolecules</i> , 2019, 126, 229-237.	7.5	47
5	A Heparan Sulfate Device for the Regeneration of Osteochondral Defects. <i>Tissue Engineering - Part A</i> , 2019, 25, 352-363.	3.1	15
6	Tilapia and human CLIC2 structures are highly conserved. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 1752-1757.	2.1	4
7	Proteobacterial Origin of Protein Arginine Methylation and Regulation of Complex I Assembly by MidA. <i>Cell Reports</i> , 2018, 24, 1996-2004.	6.4	10
8	Affinity Selection of FGF2-Binding Heparan Sulfates for Ex Vivo Expansion of Human Mesenchymal Stem Cells. <i>Journal of Cellular Physiology</i> , 2017, 232, 566-575.	4.1	27
9	Mechanisms of <i>Yersinia</i> YopO kinase substrate specificity. <i>Scientific Reports</i> , 2017, 7, 39998.	3.3	10
10	Avathrin: a novel thrombin inhibitor derived from a multicopy precursor in the salivary glands of the ixodid tick, <i>Amblyomma variegatum</i> . <i>FASEB Journal</i> , 2017, 31, 2981-2995.	0.5	14
11	<i>Yersinia</i> effector protein (YopO)-mediated phosphorylation of host gelsolin causes calcium-independent activation leading to disruption of actin dynamics. <i>Journal of Biological Chemistry</i> , 2017, 292, 8092-8100.	3.4	13
12	Functional characterization of selective exosite-binding inhibitors of matrix metalloproteinase-13 (MMP-13) – experimental validation in human breast and colon cancer. <i>Bioscience, Biotechnology and Biochemistry</i> , 2016, 80, 2122-2131.	1.3	7
13	A C9ORF72/SMCR8-containing complex regulates ULK1 and plays a dual role in autophagy. <i>Science Advances</i> , 2016, 2, e1601167.	10.3	210
14	Molecular basis for specific viral RNA recognition and 2'-O-ribose methylation by the dengue virus nonstructural protein 5 (NS5). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14834-14839.	7.1	89
15	Structural determinants of heparin-transforming growth factor- $\beta$ 1 interactions and their effects on signaling. <i>Glycobiology</i> , 2015, 25, 1491-1504.	2.5	38
16	Discovery of <i>Mycobacterium tuberculosis</i> $\beta$ -1,4-Glucan Branching Enzyme (GlgB) Inhibitors by Structure- and Ligand-based Virtual Screening. <i>Journal of Biological Chemistry</i> , 2015, 290, 76-89.	3.4	18
17	A Crystal Structure of the Dengue Virus NS5 Protein Reveals a Novel Inter-domain Interface Essential for Protein Flexibility and Virus Replication. <i>PLoS Pathogens</i> , 2015, 11, e1004682.	4.7	180
18	Plant immunophilins: a review of their structure-function relationship. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2015, 1850, 2145-2158.	2.4	38

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19	Flexibility of NS5 Methyltransferase-Polymerase Linker Region Is Essential for Dengue Virus Replication. <i>Journal of Virology</i> , 2015, 89, 10717-10721.	3.4	41
20	Investigating the Molecular Basis of Siah1 and Siah2 E3 Ubiquitin Ligase Substrate Specificity. <i>PLoS ONE</i> , 2014, 9, e106547.	2.5	17
21	Structure of a Diguanylate Cyclase from <i>Thermotoga maritima</i> : Insights into Activation, Feedback Inhibition and Thermostability. <i>PLoS ONE</i> , 2014, 9, e110912.	2.5	22
22	Hibiscus Chlorotic Ringspot Virus Coat Protein Is Essential for Cell-to-Cell and Long-Distance Movement but Not for Viral RNA Replication. <i>PLoS ONE</i> , 2014, 9, e113347.	2.5	11
23	H <sub>2</sub> O <sub>2</sub> Inhibits ABA-Signaling Protein Phosphatase HAB1. <i>PLoS ONE</i> , 2014, 9, e113643.	2.5	25
24	Identification and molecular characterization of human antibody fragments specific for dengue NS5 protein. <i>Virus Research</i> , 2014, 179, 225-230.	2.2	21
25	&#945;-Glucan Pathway as a Novel Mtb Drug Target: Structural Insights and Cues for Polypharmacological Targeting of GlgB and GlgE. <i>Current Medicinal Chemistry</i> , 2014, 21, 4074-4084.	2.4	3
26	Structural and Functional Studies of trans-Encoded HLA-DQ2.3 (DQA1*03:01/DQB1*02:01) Protein Molecule. <i>Journal of Biological Chemistry</i> , 2012, 287, 13611-13619.	3.4	63
27	Crystal Structure of Arabidopsis Cyclophilin38 Reveals a Previously Uncharacterized Immunophilin Fold and a Possible Autoinhibitory Mechanism. <i>Plant Cell</i> , 2012, 24, 2666-2674.	6.6	42
28	Enzymatic catalysis of anti-Baldwin ring closure in polyether biosynthesis. <i>Nature</i> , 2012, 483, 355-358.	27.8	117
29	Crystal structure of mouse RhoA:GTP $\gamma$ S complex in a centered lattice. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 241-245.	1.2	7
30	Validation of Drug-Like Inhibitors against Mycobacterium Tuberculosis L-Aspartate $\pm$ -Decarboxylase Using Nuclear Magnetic Resonance ( <sup>1</sup> H NMR). <i>PLoS ONE</i> , 2012, 7, e45947.	2.5	10
31	Interaction of Mycobacterium tuberculosis RshA and SigH Is Mediated by Salt Bridges. <i>PLoS ONE</i> , 2012, 7, e43676.	2.5	14
32	Frequency distribution of the reduced unit cells of centred lattices from the Protein Data Bank. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2012, 68, 295-297.	0.3	1
33	Chemoinformatic Identification of Novel Inhibitors against Mycobacterium tuberculosis L-aspartate $\pm$ -decarboxylase. <i>PLoS ONE</i> , 2012, 7, e33521.	2.5	15
34	Structure of Hibiscus Latent Singapore Virus by Fiber Diffraction: A Nonconserved His122 Contributes to Coat Protein Stability. <i>Journal of Molecular Biology</i> , 2011, 406, 516-526.	4.2	8
35	Crystal Structure of Thrombin in Complex with S-Variagin: Insights of a Novel Mechanism of Inhibition and Design of Tunable Thrombin Inhibitors. <i>PLoS ONE</i> , 2011, 6, e26367.	2.5	40
36	Crystal Structure of the PAC1R Extracellular Domain Unifies a Consensus Fold for Hormone Recognition by Class B G-Protein Coupled Receptors. <i>PLoS ONE</i> , 2011, 6, e19682.	2.5	58

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37	Structural Basis for Hormone Recognition by the Human CRFR2 $\pm$ G Protein-coupled Receptor. Journal of Biological Chemistry, 2010, 285, 40351-40361.	3.4	73
38	Crystal Structure of Full-length Mycobacterium tuberculosis H37Rv Glycogen Branching Enzyme. Journal of Biological Chemistry, 2010, 285, 20897-20903.	3.4	67
39	Modifying the Substrate Specificity of Carinoscorpis rotundicauda Serine Protease Inhibitor Domain 1 to Target Thrombin. PLoS ONE, 2010, 5, e15258.	2.5	6
40	Lack of TNF $\pm$ expression protects anaplastic lymphoma kinase-positive T-cell lymphoma (ALK+ TCL) cells from apoptosis. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15843-15848.	7.1	19
41	Structural basis of typhoid: <i>Salmonella typhi</i> type IVb pilin (PilS) and cystic fibrosis transmembrane conductance regulator interaction. Proteins: Structure, Function and Bioinformatics, 2009, 77, 253-261.	2.6	284
42	Crystal Structure of the Polyextremophilic $\pm$ -Amylase AmyB from Halothermothrix orenii: Details of a Productive Enzyme-Substrate Complex and an N Domain with a Role in Binding Raw Starch. Journal of Molecular Biology, 2008, 378, 852-870.	4.2	80
43	Structural and pharmacological comparison of daboiatoxin from <i>Daboia russelli siamensis</i> with viperotoxin F and vipoxin from other vipers. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 722-729.	2.5	13
44	Crystal structure of AmyA lacks acidic surface and provide insights into protein stability at poly-extreme condition. FEBS Letters, 2006, 580, 2646-2652.	2.8	64
45	Structural comparison of oxidized and reduced FKBP13 from Arabidopsis thaliana. Proteins: Structure, Function and Bioinformatics, 2006, 65, 789-795.	2.6	20
46	Crystal structure of uncleaved L-aspartate- $\pm$ -decarboxylase from Mycobacterium tuberculosis. Proteins: Structure, Function and Bioinformatics, 2006, 65, 796-802.	2.6	34
47	Structure and function comparison of Micropechis ikaheka snake venom phospholipase A2 isoenzymes. FEBS Journal, 2005, 272, 1211-1220.	4.7	14
48	Structural analysis uncovers a role for redox in regulating FKBP13, an immunophilin of the chloroplast thylakoid lumen. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13945-13950.	7.1	97
49	A Dimerized Coiled-Coil Domain and an Adjoining Part of Geminin Interact with Two Sites on Cdt1 for Replication Inhibition. Molecular Cell, 2004, 15, 245-258.	9.7	73
50	Expression, crystallization and preliminary X-ray analysis of isomaltulose synthase (Pall) from <i>Klebsiella</i> sp. LX3. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 150-151.	2.5	4
51	Crystallization of a novel $\pm$ -amylase, AmyB, from the thermophilic halophile <i>Halothermothrix orenii</i> . Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 2257-2258.	2.5	8
52	A HEX-1 crystal lattice required for Woronin body function in <i>Neurospora crassa</i> . Nature Structural and Molecular Biology, 2003, 10, 264-270.	8.2	77
53	A motif rich in charged residues determines product specificity in isomaltulose synthase. FEBS Letters, 2003, 534, 151-155.	2.8	23
54	Isomaltulose Synthase (Pall) of <i>Klebsiella</i> sp. LX3. Journal of Biological Chemistry, 2003, 278, 35428-35434.	3.4	56

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55	Crystallization of an $\alpha$ -amylase, AmyA, from the thermophilic halophile <i>Halothermothrix orenii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2125-2126.	2.5	9
56	Crystal structure of the CDK4/6 inhibitory protein p18INK4c provides insights into ankyrin-like repeat structure/function and tumor-derived p16INK4 mutations. <i>Nature Structural Biology</i> , 1998, 5, 74-81.	9.7	80
57	Crystal structure of a P18INK4c-DNA complex reveals a novel mechanism for DNA recognition by a protein containing a Zn <sub>2</sub> Cys <sub>6</sub> binuclear cluster. <i>Nature Structural Biology</i> , 1997, 4, 751-759.	9.7	87